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EXAMINER	
THOMAS, DAVID C	

ART UNIT	PAPER NUMBER
1637	

DATE MAILED: 06/06/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/602,837	SHI ET AL.	
	Examiner	Art Unit	
	David C. Thomas	1637	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *18 April 2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-46* is/are pending in the application.

4a) Of the above claim(s) *23-46* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-22* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *06 November 2003*. 07 January 2005
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

1. Applicant's election with traverse of Group I, claims 1-22 in the reply filed on April 18, 2006 is acknowledged. Claims 23-46 are withdrawn from further prosecution. The traversal is on the grounds that the claims are closely related and there is no burden searching all of the groups. This is not found persuasive for several reasons. First, the separate classification of the different groups is prima facie evidence of burden, which evidence has been rebutted. Second, the search for the product claims is an entirely distinct search from the method claims, since the prior art which may be used to reject product claims are often entirely unrelated references which share common products.

The requirement is still deemed proper and is therefore made FINAL.

Claim Rejections - 35 USC § 102

2. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

3. Claims 1, 2, 4, 7-11, and 14-16 are rejected under 35 U.S.C. 102(b) as being anticipated by Schmidt et al., (U.S. Patent No. 5,792,613).

Schmidt teaches a method of identifying RNA ligands which bind to a target molecule (ligand binding of nucleic acids by shape recognition, column 2, lines 17-22), said method comprising:

treating a first pool of RNA ligands that collectively bind more than one target under conditions effective to reduce the concentration or eliminate the presence of one or more predominate target-binding RNA ligands from the first pool of RNA ligands (contacting RNA population with both blocking agent and selecting nucleic acid molecule and separating non-complexed RNA from complexed population to enrich for the RNA aptamer of interest, column 2, line 63 to column 3, line 20);

amplifying the RNA ligands in the treated first pool, thereby forming a second pool of RNA ligands that is enriched in one or more non-predominate target-binding RNA ligands of the first pool but not the one or more predominate target-binding RNA ligands thereof (after each round, selected RNA population enriched for RNA aptamer, is reverse transcribed to cDNA, amplified, and transcribed back to RNA before next round, column 3, lines 28-32); and

identifying from the second pool one or more predominate target-binding RNA ligands that are present in the second pool at a higher concentration than other target-binding RNA ligands (cDNA is sequenced to identify enriched aptamer, column 3, lines 32-36).

With regard to claim 2, Schmidt teaches a method further comprising:

treating the second pool under conditions effective to reduce the concentration or eliminate the presence of one or more predominate target-binding RNA ligands (process is repeated a second round by contacting RNA population with selecting nucleic acid molecule and separating non-complexed RNA from complexed population to enrich for the RNA aptamer of interest, column 3, lines 11-25);

amplifying the RNA ligands in the treated second pool, thereby forming a third pool of RNA ligands that is enriched in one or more non-predominate target-binding RNA ligands of the second pool but not the one or more predominate target-binding RNA ligands thereof (after the first and succeeding rounds, selected RNA population enriched for RNA aptamer of interest, is reverse transcribed to cDNA, amplified, and transcribed back to RNA before next round, column 3, lines 28-32); and

identifying from the third pool one or more predominate target-binding RNA ligands that are present in the third pool at a higher concentration than other target-binding RNA ligands (for second and succeeding rounds, cDNA is sequenced to identify enriched aptamer among predominate aptamers, column 3, lines 32-36).

With regard to claim 4, Schmidt teaches a method further comprising repeating said treating, amplifying, and identifying for each subsequent pool until substantially all of the non-predominate target-binding RNA ligands in the first pool have been identified (repeating treatment, amplification and identification by sequencing to yield a detectable amount of aptamer of interest, column 3, lines 21-25 and lines 28-36).

With regard to claim 7, Schmidt teaches a method wherein each said identifying comprises:

isolating the one or more predominate target-binding RNA ligands (by separating non-complexed RNA from complexed population to enrich for the RNA aptamer of interest, whereby the non-complexed RNA will contain predominate target-binding ligands such as those binding to the blocking oligonucleotide or overlapping

oligonucleotides, column 3, lines 16-17 and column 6, lines 8-24, but not those binding by shape recognition, column 5, lines 38-54) and

sequencing the one or more predominate target-binding RNA ligands (for each round of selection, cDNA is sequenced to identify enriched aptamer, column 3, lines 32-36).

With regard to claim 8, Schmidt teaches a method wherein said identifying comprises:

isolating the one or more predominate target-binding RNA ligands (by separating non-complexed RNA from complexed population to enrich for the RNA aptamer of interest, whereby the non-complexed RNA will contain predominate target-binding ligands such as those binding to the blocking oligonucleotide or overlapping oligonucleotides, column 3, lines 16-17 and column 6, lines 8-24, but not those binding by shape recognition, column 5, lines 38-54) and

sequencing the one or more predominate target-binding RNA ligands (after first round of selection, cDNA is sequenced to identify enriched aptamer, column 3, lines 32-36).

With regard to claim 9, Schmidt teaches a method further comprising:

preparing the pool of RNA ligands that collectively bind to more than one target (contacting RNA population made from randomized DNA library, column 5, lines 22-26, with both blocking agent and selecting nucleic acid molecule, column 2, line 63 to column 3, line 15);

identifying one or more predominate target-binding RNA ligands (by separating non-complexed RNA from complexed population to enrich for the RNA aptamer of interest, whereby the non-complexed RNA will contain predominate target-binding ligands such as those binding to the blocking oligonucleotide or overlapping oligonucleotides, column 3, lines 16-17 and column 6, lines 8-24, but not those binding by shape recognition, column 5, lines 38-54).

With regard to claim 10, Schmidt teaches a method wherein said preparing comprises:

expressing a library of RNA molecules that includes both RNA ligands that bind to at least one of one or more targets and RNA molecules that do not bind any of the one or more targets (RNA population can be a randomized, synthetic RNA library, column 3, lines 26-28); and

partitioning the library of RNA molecules to form the first pool of RNA ligands (partitioning by contacting RNA population with both blocking agent and selecting nucleic acid molecule and separating non-complexed RNA from complexed population to enrich for the RNA aptamer of interest, column 2, line 63 to column 3, line 20).

With regard to claim 11, Schmidt teaches a method wherein said expressing the library of RNA molecules comprises:

expressing a library of DNA molecules that includes both DNA ligands that bind to at least one of one or more targets and DNA molecules that do not bind any of the one or more targets (random synthetic library of DNA is constructed, column 19-25); and

transcribing the library of RNA molecules from the library of DNA molecules (DNA library is transcribed into RNA population, column 25-29).

With regard to claim 14, Schmidt teaches a method wherein the targets comprise natural or synthetic small molecules, macromolecules, supramolecular assemblies, and combinations thereof (target is an RNA molecule containing selected structural element and is synthesized by transcription of synthetic DNA or cDNA, column 5, lines 9-15).

With regard to claim 15, Schmidt teaches a method of reducing the concentration or eliminating the presence of unwanted target-binding species from a pool of RNA ligands, said method comprising:

providing a pool of RNA ligands which includes both wanted and unwanted target-binding RNA ligands (contacting RNA population made from randomized DNA library, column 5, lines 22-26, with both blocking agent and selecting nucleic acid molecule, column 2, line 63 to column 3, line 15);

identifying one or more unwanted target-binding RNA ligands (by separating non-complexed RNA from complexed population to enrich for the RNA aptamer of interest, whereby the non-complexed RNA will contain predominate target-binding ligands such as those binding to the blocking oligonucleotide or overlapping oligonucleotides, column 3, lines 16-17 and column 6, lines 8-24, but not those binding by shape recognition, column 5, lines 38-54); and

treating the pool under conditions effective to reduce the concentration or eliminate the presence of the one or more unwanted target-binding RNA ligands from

the pool of RNA ligands (unwanted target RNA ligands can be removed by separation techniques such as affinity chromatography, column 6, lines 39-60).

With regard to claim 16, Schmidt teaches a method wherein said identifying comprises:

isolating the one or more unwanted target-binding RNA ligands (by separating non-complexed RNA from complexed population to enrich for the RNA aptamer of interest, whereby the non-complexed RNA will contain predominate target-binding ligands such as those binding to the blocking oligonucleotide or overlapping oligonucleotides, column 3, lines 16-17 and column 6, lines 8-24, but not those binding by shape recognition, column 5, lines 38-54) and

sequencing the one or more unwanted target-binding RNA ligands (cDNA is sequenced to identify enriched aptamer, column 3, lines 32-36).

4. Claims 1, 2, 4, 7-11, and 14-16 are rejected under 35 U.S.C. 102(b) as being anticipated by Toole et al., (U.S. Patent No. 5,582,981).

Toole teaches a method of identifying RNA ligands which bind to a target molecule (oligomer binding of target biomolecules, abstract and column 2, lines 56-64), said method comprising:

treating a first pool of RNA ligands that collectively bind more than one target under conditions effective to reduce the concentration or eliminate the presence of one or more predominate target-binding RNA ligands from the first pool of RNA ligands (contacting random oligomer population with target substance coupled to support and removing unbound members of mixture to enrich for the RNA aptamer of interest,

column 2, line 65 to column 3, line 9; oligomers include RNA or DNA, column 4, lines 18-25);

amplifying the RNA ligands in the treated first pool, thereby forming a second pool of RNA ligands that is enriched in one or more non-predominate target-binding RNA ligands of the first pool but not the one or more predominate target-binding RNA ligands thereof (amplifying the recovered oligonucleotides, column 3, lines 9-10); and

identifying from the second pool one or more predominate target-binding RNA ligands that are present in the second pool at a higher concentration than other target-binding RNA ligands (sequencing the recovered and amplified oligonucleotides to identify enriched aptamer, column 3, lines 10-12).

With regard to claim 2, Toole teaches a method further comprising:

treating the second pool under conditions effective to reduce the concentration or eliminate the presence of one or more predominate target-binding RNA ligands (process is repeated a second round by contacting random oligomer population with target substance coupled to support and removing unbound members of mixture to enrich for the RNA aptamer of interest, column 2, line 65 to column 3, line 9 and column 8, lines 41-43);

amplifying the RNA ligands in the treated second pool, thereby forming a third pool of RNA ligands that is enriched in one or more non-predominate target-binding RNA ligands of the second pool but not the one or more predominate target-binding RNA ligands thereof (after the first and succeeding rounds, selected RNA population

enriched for RNA aptamer of interest, is amplified, and transcribed back to RNA before next round, column 8, lines 31-43); and

identifying from the third pool one or more predominate target-binding RNA ligands that are present in the third pool at a higher concentration than other target-binding RNA ligands (after 3-6 rounds, amplified sequences can be cloned and sequenced to identify enriched ligands among predominate ligands, and to identify consensus sequences among aptamers, column 8, lines 48-58).

With regard to claim 4, Toole teaches a method further comprising repeating said treating, amplifying, and identifying for each subsequent pool until substantially all of the non-predominate target-binding RNA ligands in the first pool have been identified (repeating treatment, amplification and identification by sequencing to yield individual, distinct aptamers, column 8, lines 31-54).

With regard to claim 7, Toole teaches a method wherein each said identifying comprises:

isolating the one or more predominate target-binding RNA ligands (column 7, lines 59-67; predominate species will be the dominant species in early rounds, but will be gradually lost with each round of selection, since the specific, non-predominate species in enriched about 1,000-fold each round, column 8, lines 25-30) and

sequencing the one or more predominate target-binding RNA ligands (amplified sequences can be cloned and sequenced to identify enriched ligands among predominate ligands, column 8, lines 48-54).

With regard to claim 8, Toole teaches a method wherein said identifying comprises:

isolating the one or more predominate target-binding RNA ligands (column 7, lines 59-67; by separating unbound oligomers from complexed population to enrich for the RNA aptamer of interest among the predominate ligands, with 1,000-fold enrichment at each round, column 8, lines 25-30) and

sequencing the one or more predominate target-binding RNA ligands (amplified sequences can be cloned and sequenced to identify enriched ligands among predominate ligands, column 8, lines 48-54).

With regard to claim 9, Toole teaches a method further comprising:

preparing the pool of RNA ligands that collectively bind to more than one target (population of oligomers made from randomized sequences, column 7, lines 15-24);

identifying one or more predominate target-binding RNA ligands (amplified sequences can be cloned and sequenced to identify enriched ligands among predominate ligands, column 8, lines 48-54).

With regard to claim 10, Toole teaches a method wherein said preparing comprises:

expressing a library of RNA molecules that includes both RNA ligands that bind to at least one of one or more targets and RNA molecules that do not bind any of the one or more targets (RNA population can be made from pool of random DNA oligomers by transcription, column 7, lines 15-24); and

partitioning the library of RNA molecules to form the first pool of RNA ligands (partitioning by contacting RNA population with target coupled to solid support and separating unbound oligomers from bound population to enrich for the RNA aptamer of interest, column 7, lines 59-67).

With regard to claim 11, Toole teaches a method wherein said expressing the library of RNA molecules comprises:

expressing a library of DNA molecules that includes both DNA ligands that bind to at least one of one or more targets and DNA molecules that do not bind any of the one or more targets (pool of random DNA oligomers is generated using conventional synthesis techniques, column 7, lines 15-20); and

transcribing the library of RNA molecules from the library of DNA molecules (RNA population can be made from pool of random DNA oligomers by transcription, column 7, lines 15-24).

With regard to claim 14, Toole teaches a method wherein the targets comprise natural or synthetic small molecules, macromolecules, supramolecular assemblies, and combinations thereof (targets include polypeptides, short peptides, lipids, glycolipids, phospholipids, leukotrienes, glycoproteins, carbohydrates, or cell surface molecules, column 3, lines 58-64).

With regard to claim 15, Toole teaches a method of reducing the concentration or eliminating the presence of unwanted target-binding species from a pool of RNA ligands, said method comprising:

providing a pool of RNA ligands which includes both wanted and unwanted target-binding RNA ligands (contacting oligomer population made from randomized DNA sequences, column 5, lines 15-24);

identifying one or more unwanted target-binding RNA ligands (contacting oligomers with target substance coupled to support and removing unbound members of mixture to enrich for the RNA aptamer of interest, column 2, line 65 to column 3, line 9; oligomers include RNA or DNA, column 4, lines 18-25); and

treating the pool under conditions effective to reduce the concentration or eliminate the presence of the one or more unwanted target-binding RNA ligands from the pool of RNA ligands (unwanted target RNA ligands can be removed by separation techniques such as affinity chromatography, column 7, lines 59-67; the specific, non-predominate species in enriched about 1,000 fold each round, column 8, lines 25-30).

With regard to claim 16, Toole teaches a method wherein said identifying comprises:

isolating the one or more unwanted target-binding RNA ligands (unwanted target RNA ligands can be removed by separation techniques such as affinity chromatography, column 7, lines 59-67; the specific, non-predominate species in enriched about 1,000-fold each round, column 8, lines 25-30) and

sequencing the one or more unwanted target-binding RNA ligands (amplified sequences can be cloned and sequenced to identify enriched ligands among predominate ligands, column 8, lines 48-54).

Claim Rejections - 35 USC § 103

5. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

6. This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

7. Claims 3, 5, 6, 12, 13, and 17-22 are rejected under 35 U.S.C. 103(a) as being unpatentable over Schmidt et al., (U.S. Patent No. 5,792,613) in view of Rabin et al., (U.S. Patent No. 6,344,321).

Schmidt teaches the limitations of claims 1, 2, 4, 7-11, and 14-16 as discussed above.

Schmidt does not teach a method of identifying RNA ligands which bind to a target molecule, comprising introducing into the pool to be treated one or more nucleic acid molecules that hybridize to the one or more predominate target-binding RNA ligands to form hybrid complexes and introducing into the pool to be treated an enzyme

which cleaves at least the RNA ligand of the hybrid complexes, thereby destroying the one or more predominate target-binding RNA ligands, wherein the enzyme is RNaseH. Schmidt also does not teach a method wherein unwanted RNA ligands are bound to a nitrocellulose matrix, and are contacted with a DNA molecule to form hybrid complexes, which are destroyed upon addition of RNaseH.

With regard to claims 3, 5, 12, and 17, Rabin teaches a method wherein each said treating comprises:

introducing into the pool to be treated one or more nucleic acid molecules that hybridize to target-binding RNA ligands to form hybrid complexes (hybridization of DNA cleavage primers to RNA ligands and Figure 2, top) and

introducing into the pool to be treated an enzyme which cleaves at least the RNA ligand of the hybrid complexes, thereby removing unwanted RNA sequences (DNA:RNA hybrids are cleaved upon addition of RNaseH to remove or truncate unwanted RNA sequences, column 15, lines 8-11 and Figure 2, bottom with cleavage sites indicated at top).

With regard to claims 6, 13, and 18, Rabin teaches a method wherein the one or more nucleic acid molecules are DNA (cleavage primers, SEQ ID Nos. 9 and 10, and Figure 2, top) and the enzyme is an RNaseH enzyme (column 5, lines 47-55 and column 15, lines 8-11).

With regard to claim 19, Rabin teaches a method wherein the one or more unwanted target-binding RNA ligands comprise one or more RNA ligands that bind to a matrix used to partition the pool of RNA ligands from a library of RNA molecules

(nitrocellulose filters can be used to bind aptamers during partitioning from nucleic acids that do not interact with target, column 12, lines 13-23).

With regard to claim 20, Rabin teaches a method wherein the unwanted target-binding RNA ligands are portions of RNA ligands that bind to a matrix (fixed sequences of RNA, column 15, lines 9-10 and Figure 2, top), and wherein said treating comprises:

introducing into the pool one or more nucleic acid molecules that hybridize to the RNA ligands that bind to a matrix, thereby forming hybrid complexes (hybridization of DNA cleavage primers to RNA ligands and Figure 2, top) and

introducing into the pool an enzyme which cleaves at least portions of the RNA ligands of the hybrid complexes, thereby removing these portions of the RNA ligands that bind to a matrix (DNA:RNA hybrids are cleaved upon addition of RNaseH to remove or truncate unwanted RNA sequences, column 15, lines 8-11 and Figure 2, bottom with cleavage sites indicated at top).

With regard to claim 21, Rabin teaches a method wherein the one or more nucleic acid molecules are DNA and the enzyme is an RNaseH enzyme (cleavage primers, SEQ ID Nos. 9 and 10, and Figure 2, top) and the enzyme is an RNaseH enzyme (column 5, lines 47-55 and column 15, lines 8-11).

With regard to claim 22, Rabin teaches a method wherein the matrix is a nitrocellulose matrix (nitrocellulose filters are used to bind target molecules and target/ligand complexes for partitioning from non-binding members of the RNA mixture, column 12, lines 13-23).

It would have been prima facie obvious to one having ordinary skill in the art at the time the invention was made to combine the method of Schmidt for identifying RNA ligands which bind to a target molecule with those of Rabin for selectively removing RNA sequences from a population of RNA molecules being screened as potential aptamers, since this method is highly efficient for removing specific sequences that may be unwanted in the final aptamer preparation. Thus, an ordinary practitioner would have been motivated to use methods of RNA removal as taught by Rabin since specific RNA sequences can be easily targeted for removal by designing DNA primers to remove portions of the RNA, such as for truncating fixed sequences (Rabin, column 15, lines 4-10 and Figure 2, top), or for complete removal by using a series of primers for the entire molecule. The cleavage reaction using RNaseH could be performed in solution prior to partitioning (Rabin, column 15, lines 4-13) or when the aptamers are bound to nitrocellulose filters (Rabin, column 12, lines 13-23) or affinity columns (Schmidt, column column 6, lines 39-60).

Conclusion

8. Claims 1-22 are rejected. No claims are allowable.

Correspondence

9. Any inquiry concerning this communication or earlier communications from the examiner should be directed to David C. Thomas whose telephone number is 571-272-3320. The examiner can normally be reached on 5 days, 9-5:30.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached on 571-272-0782. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

David C. Thomas 6/1/06
Patent Examiner
Art Unit 1637

JEFFREY FREDMAN
PRIMARY EXAMINER
6/1/06